OIPE

RAW SEQUENCE LISTING   DATE: 07/18/2001
PATENT APPLICATION: US/09/898,456   TIME: 12:46:48

Input Set : **A:\LEX-0198-USA SEQUENCE LISTING.txt**
Output Set: **N:\CRF3\07182001\I898456.raw**

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 4 <110> APPLICANT: Friddle, Carl Johan
 5        Hilbun, Erin
 6        Scoville, John
 7        Walke, D. Wade
 9 <120> TITLE OF INVENTION: Novel Human Secreted Signal Proteins and Polynucleotides
Encoding the
10        Same
12 <130> FILE REFERENCE: LEX-0198-USA
C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/898,456
C--> 14 <141> CURRENT FILING DATE: 2002-07-03
14 <150> PRIOR APPLICATION NUMBER: US 60/216,384
15 <151> PRIOR FILING DATE: 2000-07-07
17 <150> PRIOR APPLICATION NUMBER: US 60/219,890
18 <151> PRIOR FILING DATE: 2000-07-21
20 <150> PRIOR APPLICATION NUMBER: US 60/230,609
21 <151> PRIOR FILING DATE: 2000-09-06
23 <160> NUMBER OF SEQ ID NOS: 24
25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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28 <211> LENGTH: 1272
29 <212> TYPE: DNA
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35 ctgtgtgcca gcatcccggg cctggtcccc aagcagctcc gcttctgcag gaactacgtg    180
36 gagatcatgc ccagcgtggc cgagggcatc aagattggca tccaggagtg ccagcaccag    240
37 ttccgcggcc gccggtggaa ctgcaccacc gtccacgaca gcctggccat cttcgggccc    300
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39 gcctttgcag tgacacgctc atgtgcagaa ggcacggccg ccatctgtgg ctgcagcagc    420
40 cgccaccagg gctcaccagg caagggctgg aagtggggtg gctgtagcga ggacatcgag    480
41 tttggtggga tggtgtctcg ggagttcgcc gacgcccggg agaaccggcc agatgcccgc    540
42 tcagccatga accgccacaa caacgaggct gggcgccagg ccatcgccag ccacatgcac    600
43 ctcaagtgca gtgccacgg gctgtcgggc agctgcgagg tgaagacatg ctggtggtcg    660
44 caacccgact tccgcgccat cggtgacttc ctcaaggaca agtacgacag cgcctcggag    720
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48 tcgcacggca tcgacggctg cgacctgctg tgctgcggcc gcggccacaa cgcgcgagcg    960
49 gagcggcgcc gggagaagtg ccgctgcgtg ttccactggt gctgctacgt cagctgccag   1020
50 gagtgcacgc gcgtctacga cgtgcacacc tgcaaggatg gatgcctcag gacagggcac   1080
51 tcaggtccct gtcggagtct tgcttggatc tggagccctg atcccagggg gcatgacctc   1140
52 ctggagcaac ttccaaggtc tgggggacta ggtcagtgtt cctccctgca gaactggact   1200
53 gctgtcagtg gctgccttcg ggatcatctg ggagggcttc caggaggagg tgagcatggg   1260
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57 <211> LENGTH: 423
58 <212> TYPE: PRT
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 65             20                  25                  30
 66 Ser Ser Leu Gly Ser Gln Pro Ile Leu Cys Ala Ser Ile Pro Gly Leu
 67         35                  40                  45
 68 Val Pro Lys Gln Leu Arg Phe Cys Arg Asn Tyr Val Glu Ile Met Pro
 69     50                  55                  60
 70 Ser Val Ala Glu Gly Ile Lys Ile Gly Ile Gln Glu Cys Gln His Gln
 71 65                  70                  75                  80
 72 Phe Arg Gly Arg Arg Trp Asn Cys Thr Thr Val His Asp Ser Leu Ala
 73             85                  90                  95
 74 Ile Phe Gly Pro Val Leu Asp Lys Ala Thr Arg Glu Ser Ala Phe Val
 75             100                 105                 110
 76 His Ala Ile Ala Ser Ala Gly Val Ala Phe Ala Val Thr Arg Ser Cys
 77         115                 120                 125
 78 Ala Glu Gly Thr Ala Ala Ile Cys Gly Cys Ser Ser Arg His Gln Gly
 79     130                 135                 140
 80 Ser Pro Gly Lys Gly Trp Lys Trp Gly Gly Cys Ser Glu Asp Ile Glu
 81 145                 150                 155                 160
 82 Phe Gly Gly Met Val Ser Arg Glu Phe Ala Asp Ala Arg Glu Asn Arg
 83             165                 170                 175
 84 Pro Asp Ala Arg Ser Ala Met Asn Arg His Asn Asn Glu Ala Gly Arg
 85             180                 185                 190
 86 Gln Ala Ile Ala Ser His Met His Leu Lys Cys Lys Cys His Gly Leu
 87         195                 200                 205
 88 Ser Gly Ser Cys Glu Val Lys Thr Cys Trp Trp Ser Gln Pro Asp Phe
 89     210                 215                 220
 90 Arg Ala Ile Gly Asp Phe Leu Lys Asp Lys Tyr Asp Ser Ala Ser Glu
 91 225                 230                 235                 240
 92 Met Val Val Glu Lys His Arg Glu Ser Arg Gly Trp Val Glu Thr Leu
 93             245                 250                 255
 94 Arg Pro Arg Tyr Thr Tyr Phe Lys Val Pro Thr Glu Arg Asp Leu Val
 95             260                 265                 270
 96 Tyr Tyr Glu Ala Ser Pro Asn Phe Cys Glu Pro Asn Pro Glu Thr Gly
 97         275                 280                 285
 98 Ser Phe Gly Thr Arg Asp Arg Thr Cys Asn Val Ser Ser His Gly Ile
 99     290                 295                 300
100 Asp Gly Cys Asp Leu Leu Cys Cys Gly Arg Gly His Asn Ala Arg Ala
101 305                 310                 315                 320
102 Glu Arg Arg Arg Glu Lys Cys Arg Cys Val Phe His Trp Cys Cys Tyr
103             325                 330                 335
104 Val Ser Cys Gln Glu Cys Thr Arg Val Tyr Asp Val His Thr Cys Lys
105             340                 345                 350
106 Asp Gly Cys Leu Arg Thr Gly His Ser Gly Pro Cys Arg Ser Leu Ala
107             355                 360                 365
108 Trp Ile Trp Ser Pro Gly Ser Gln Gly His Asp Leu Leu Glu Gln Leu
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110 Pro Arg Ser Gly Gly Leu Gly Gln Cys Ser Ser Leu Gln Asn Trp Thr
111 385                   390                  395                400
112 Ala Val Ser Gly Cys Leu Arg Asp His Leu Gly Gly Leu Pro Gly Gly
113                   405                  410                415
114 Gly Glu His Gly Asp Thr Ser
115               420
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118 <211> LENGTH: 1059
119 <212> TYPE: DNA
120 <213> ORGANISM: homo sapiens
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125 ctgtgtgcca gcatcccggg cctggtcccc aagcagctcc gcttctgcag gaactacgtg     180
126 gagatcatgc ccagcgtggc cgagggcatc aagattggca tccaggagtg ccagcaccag     240
127 ttccgcggcc gccggtggaa ctgcaccacc gtccacgaca gcctggccat cttcgggccc     300
128 gtgctggaca aagctaccag ggagtcggcc tttgtccacg ccattgcctc agccggtgtg     360
129 gcctttgcag tgacacgctc atgtgcagaa ggcacggccg ccatctgtgg ctgcagcagc     420
130 cgccaccagg gctcaccagg caagggctgg aagtgggggtg ctgtagcga ggacatcgag     480
131 tttggtggga tggtgtctcg ggagttcgcc gacgcccggg agaaccggcc agatgcccgc     540
132 tcagccatga ccgccacaa caacgaggct gggcgccagg ccatcgccag ccacatgcac     600
133 ctcaagtgca agtgccacgg gctgtcgggc agctgcgagg tgaagacatg ctggtggtcg     660
134 caacccgact tccgcgccat cggtgacttc ctcaaggaca agtacgacag cgcctcggag     720
135 atggtggtgg agaagcaccg ggagtcccgc ggctgggtgg agaccctgcg gccgcgctac     780
136 acctacttca aggtgcccac ggagcgcgac ctggtctact acgaggcctc gcccaacttc     840
137 tgcgagccca accctgagac gggctccttc ggcacgcgcg accgcacctg caacgtcagc     900
138 tcgcacggca tcgacggctg cgacctgctg tgctgcggcc gcggccacaa cgcgcgagcg     960
139 gagcggcgcc gggagaagtg ccgctgcgtg ttccactggt gctgctacgt cagctgccag    1020
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143 <211> LENGTH: 352
144 <212> TYPE: PRT
145 <213> ORGANISM: homo sapiens
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150 Leu Gly Ser Tyr Pro Ile Trp Trp Ser Leu Ala Val Gly Pro Gln Tyr
151               20                  25                  30
152 Ser Ser Leu Gly Ser Gln Pro Ile Leu Cys Ala Ser Ile Pro Gly Leu
153               35                  40                  45
154 Val Pro Lys Gln Leu Arg Phe Cys Arg Asn Tyr Val Glu Ile Met Pro
155       50                  55                  60
156 Ser Val Ala Glu Gly Ile Lys Ile Gly Ile Gln Glu Cys Gln His Gln
157 65                  70                  75                  80
158 Phe Arg Gly Arg Arg Trp Asn Cys Thr Thr Val His Asp Ser Leu Ala
159               85                  90                  95
160 Ile Phe Gly Pro Val Leu Asp Lys Ala Thr Arg Glu Ser Ala Phe Val
161               100                 105                 110
```

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162 His Ala Ile Ala Ser Ala Gly Val Ala Phe Ala Val Thr Arg Ser Cys
163         115             120             125
164 Ala Glu Gly Thr Ala Ala Ile Cys Gly Cys Ser Ser Arg His Gln Gly
165     130             135             140
166 Ser Pro Gly Lys Gly Trp Lys Trp Gly Gly Cys Ser Glu Asp Ile Glu
167 145             150             155             160
168 Phe Gly Gly Met Val Ser Arg Glu Phe Ala Asp Ala Arg Glu Asn Arg
169             165             170             175
170 Pro Asp Ala Arg Ser Ala Met Asn Arg His Asn Asn Glu Ala Gly Arg
171         180             185             190
172 Gln Ala Ile Ala Ser His Met His Leu Lys Cys Lys Cys His Gly Leu
173         195             200             205
174 Ser Gly Ser Cys Glu Val Lys Thr Cys Trp Trp Ser Gln Pro Asp Phe
175     210             215             220
176 Arg Ala Ile Gly Asp Phe Leu Lys Asp Lys Tyr Asp Ser Ala Ser Glu
177 225             230             235             240
178 Met Val Val Glu Lys His Arg Glu Ser Arg Gly Trp Val Glu Thr Leu
179             245             250             255
180 Arg Pro Arg Tyr Thr Tyr Phe Lys Val Pro Thr Glu Arg Asp Leu Val
181         260             265             270
182 Tyr Tyr Glu Ala Ser Pro Asn Phe Cys Glu Pro Asn Pro Glu Thr Gly
183         275             280             285
184 Ser Phe Gly Thr Arg Asp Arg Thr Cys Asn Val Ser Ser His Gly Ile
185     290             295             300
186 Asp Gly Cys Asp Leu Leu Cys Cys Gly Arg Gly His Asn Ala Arg Ala
187 305             310             315             320
188 Glu Arg Arg Arg Glu Lys Cys Arg Cys Val Phe His Trp Cys Cys Tyr
189             325             330             335
190 Val Ser Cys Gln Glu Cys Thr Arg Val Tyr Asp Val His Thr Cys Lys
191         340             345             350
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194 <211> LENGTH: 1505
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201 ggccctccgc gccctctcgc gcggcgatgg ccccactcgg atacttctta ctcctctgca     180
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204 agctccgctt ctgcaggaac tacgtggaga tcatgcccag cgtggccgag ggcatcaaga     360
205 ttggcatcca ggagtgccag caccagttcc gcggccgccg gtggaactgc accaccgtcc     420
206 acgacagcct ggccatcttc gggcccgtgc tggacaaagc taccagggag tcggcctttg     480
207 tccacgccat gcctcagcc ggtgtggcct ttgcagtgac acgctcatgt gcagaaggca     540
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210 cccgggagaa ccggccagat gcccgctcag ccatgaaccg ccacaacaac gaggctgggc     720
211 gccaggccat cgccagccac atgcacctca agtgcaagtg ccacgggctg tcgggcagct     780
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213 aggacaagta cgacagcgcc tcggagatgg tggtggagaa gcaccgggag tcccgcggct    900
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215 tctactacga ggcctcgccc aacttctgcg agcccaaccc tgagacgggc tccttcggca   1020
216 cgcgcgaccg cacctgcaac gtcagctcgc acggcatcga cggctgcgac ctgctgtgct   1080
217 gcggccgcgg ccacaacgcg cgagcggagc ggcgccggga gaagtgccgc tgcgtgttcc   1140
218 actggtgctg ctacgtcagc tgccaggagt gcacgcgcgt ctacgacgtg cacacctgca   1200
219 aggatggatg cctcaggaca gggcactcag gtccctgtcg gagtcttgct tggatctgga   1260
220 gccctggatc ccaggggcat gacctcctgg agcaacttcc aaggtctggg ggactaggtc   1320
221 agtgttcctc cctgcagaac tggactgctg tcagtggctg ccttcgggat catctgggag   1380
222 ggcttccagg aggaggtgag catggggaca cttcctaggg ctccaacatc ctcctgtaat   1440
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228 <212> TYPE: DNA
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247 tccaggtggg agcgacgtag ctgtgggcgc ctgtgcactg agtgtgggct gcaggtggaa    960
248 gagaggaaaa ctgaggtcat aagcagctgt aactgcaaat tccagtggtg ctgtacggtc   1020
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253 <211> LENGTH: 369
254 <212> TYPE: PRT
255 <213> ORGANISM: homo sapiens
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261         20                  25                  30
262 Cys Leu Thr Phe Ser Leu Phe Gly Arg Ser Val Asn Asn Phe Leu Ile
263         35                  40                  45
264 Thr Gly Pro Lys Ala Tyr Leu Thr Tyr Thr Thr Ser Val Ala Leu Gly
265     50                  55                  60
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VERIFICATION SUMMARY   DATE: 07/18/2001
PATENT APPLICATION: **US/09/898,456**   TIME: 12:46:49

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L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date